WO 2005/085867 PCT/IB2005/000382

## PC32099A\_GPR35 SERQUENCE for NY (Identical to PC32099) SEQUENCE LISTING

```
<110>
       Pfizer Inc.; Pfizer Japan Inc. (for Japan)
<120>
       GPR35
<130>
       PC32099
<160>
       23
<170>
       PatentIn version 3.1
<210>
       921
<211>
<212>
       DNA
<213>
       rat
<400> 1
atgaacaata caaattgtag catceteeeg tggcetgetg cagteaacca catetteace
                                                                       60
atetacitgg tettgetget ggtgetggge etgetgetea atggeetgge actetgggta
                                                                      120
ttetgetate geatgeacea gtggaeggag accegagtet atatgaecaa cetggetgtg
                                                                      180
getgaegtet geetgetetg eteettgeea ttegtgetgt aeteeetgaa ataeagtaet
                                                                      240
teggacacae ecatetgeca geteteacag ggeatetace tggteaacag gtacatgage
                                                                      300
ataagettgg teacegeeat tgetgtggae egetatgtgg eagtgeggea teecetgegt
                                                                      360
geeegtgage tgeggteece aeggeagget ggageagtgt gtgtggeeet etgggtgata
                                                                      420
gtggtcacct ecetggtact gcgctggcgc ctggggatac aggagggtgg cttctgcttc
                                                                      480
ageageeaaa ateggtacaa etteageaee aetgeettet egetgetggg attetaeetg
                                                                      540
cegetggeea tagtggtett etgetetttg eaggttgtga etgegttgge eegaaggeea
                                                                      600
gccactgacg tggagcaggt ggaggccact cagaaggcca cccgcatggt ctgggccaac
                                                                      660
ttggccgtgt ttatcatctg cttcctgccc ctgcatttga tcctgacagt gcaggtctcc
                                                                      720
ctgaacetec acacetgege tgecegaaac atetteagee gtgecetgae aateacagee
                                                                      780
aageteteag acateaactg etgeetggat gecatetgtt actactacat ggecaaagag
                                                                      840
ttecaggatg cgtccttgcg ggccacagcc tctagcacac cccacaagag ccaagatact
                                                                      900
cagagectga gecteaceta g
                                                                      921
<210>
      2
       306
```

<211> PRT

<213> rat

<400>

Met Asn Asn Thr Asn Cys Ser Ile Leu Pro Trp Pro Ala Ala Val Asn 1 10 15

His Ile Phe Thr Ile Tyr Leu Val Leu Leu Leu Val Leu Gly Leu Leu 25 30

Leu Asn Gly Leu Ala Leu Trp Val Phe Cys Tyr Arg Met His Gln Trp

Thr Glu Thr Arg Val Tyr Met Thr Asn Leu Ala Val Ala Asp Val Cys 50 60

Leu Leu Cys Ser Leu Pro Phe Val Leu Tyr Ser Leu Lys Tyr Ser Thr

PC32099A\_GPR35 SERQUENCE for NY (Identical to PC32099)
75 80

Ser Asp Thr Pro I le Cys Gln Leu Ser Gln Gly I le Tyr Leu Val Asn 85 90 95

Arg Tyr Met Ser Ile Ser Leu Val Thr Ala Ile Ala Val Asp Arg Tyr 100 105 110

Val Ala Val Arg His Pro Leu Arg Ala Arg Glu Leu Arg Ser Pro Arg 115 120 125

Gln Ala Gly Ala Val Cys Val Ala Leu Trp Val Ile Val Val Thr Ser 130 135 140

Leu Val Leu Arg Trp Arg Leu Gly Ile Gl<br/>n Glu Gly Gly Phe Cys Phe 145 <br/> 150 155 <br/> 160

Ser Ser Gln Asn Arg Tyr Asn Phe Ser Thr Thr Ala Phe Ser Leu Leu 165 170 175

Gly Phe Tyr Leu Pro Leu Ala IIe Val Val Phe Cys Ser Leu Gln Val 180 185 190

Val Thr Ala Leu Ala Arg Arg Pro Ala Thr Asp Val Glu Gln Val Glu 195 200 205

Ala Thr Gln Lys Ala Thr Arg Met Val Trp Ala Asn Leu Ala Val Phe 210 220

Ile Ile Cys Phe Leu Pro Leu His Leu Ile Leu Thr Val Gln Val Ser 225 230 235 240

Leu Asn Leu His Thr Cys Ala Ala Arg Asn Ile Phe Ser Arg Ala Leu 245 250 250

Thr Ile Thr Ala Lys Leu Ser Asp Ile Asn Cys Cys Leu Asp Ala Ile 260 270

Cys Tyr Tyr Met Ala Lys Glu Phe Gln Asp Ala Ser Leu Arg Ala 275

Leu Thr 305

<210> 3

<211> 930 <212> DNA

<213> human

<400> 3
atgaatggea cetacaacae etgtggetee agegacetea cetggeecee agegateaag
etgggettet acgcetactt gggcgteetg etggtgetag geetgetget caacageetg
gegetetggg tgttetgetg ecgcatgeag cagtggaegg agaceegcat etacatgace
180

WO 2005/085867 PCT/IB2005/000382

aacctggegg	tggccgacct			RQUENCE for ccttcgtgct	NY (Identical geactecets	to PC32099) 240
cgagacacct	cagacacgcc	getgtgccag	ctctcccagg	gcatctacct	gaccaacagg	300
tacatgagca	teageetggt	catggccate	gccgtggacc	gctatgtggc	cgtgcggcac	360
ccgctgcgtg	${\tt cccgcgggct}$	geggteece	aggeaggetg	eggeegtgtg	egeggteete	420
tgggtgctgg	teateggete	cetggtgget	egetggetee	tggggattca	ggagggcggc	480
ttctgcttca	ggagcacccg	gcacaatttc	aactccatgg	egtteeeget	gctgggatte	540
tacctgcccc	tggccgtggt	ggtcttctgc	tecetgaagg	tggtgactgc	cctggcccag	600
aggccaccca	ccgacgtggg	gcaggcagag	gecaceegea	aggetgeeeg	catggtctgg	660
gccaacetee	tggtgttcgt	ggtetgette	etgeceetge	acgtggggct	gacagtgege	720
ctcgcagtgg	gctggaacgc	etgtgccete	ctggagacga	teegtegege	cctgtacata	780
accagcaage	teteagatge	caactgctgc	etggaegeea	tetgetaeta	etacatggcc	840
aaggagttee	aggaggegte	tgcactggcc	gtggetecca	gtgctaaggc	ccacaaaagc	900
caggactete	tgtgcgtgac	cctcgcctaa				930

<210> 4 <211> 309 <212> PRT

<213> human

<400> 4

Met Asn Gly Thr Tyr Asn Thr Cys Gly Ser Ser Asp Leu Thr Trp Pro  $1 \hspace{1cm} 10 \hspace{1cm} 10 \hspace{1cm} 15 \hspace{1cm}$ 

Pro Ala Ile Lys Leu Gly Phe Tyr Ala Tyr Leu Gly Val Leu Leu Val 25 30

Met Gln Gln Trp Thr Glu Thr Arg Ile Tyr Met Thr Asn Leu Ala Val 50 60

Ala Asp Leu Cys Leu Cys Thr Leu Pro Phe Val Leu His Ser Leu 65 70 75 Leu 80

Arg Asp Thr Ser Asp Thr Pro Leu Cys Gln Leu Ser Gln Gly Ile Tyr 85 90 95

Leu Thr Asn Arg Tyr Met Ser Ile Ser Leu Val Met Ala Ile Ala Val 100 105 110

Asp Arg Tyr Val Ala Val Arg His Pro Leu Arg Ala Arg Gly Leu Arg 115 125

Ser Pro Arg Gln Ala Ala Ala Val Cys Ala Val Leu Trp Val Leu Val 130 140

Ile Gly Ser Leu Val Ala Arg Trp Leu Leu Gly Ile Gln Glu Gly Gly 145 150 150 160

Phe Cys Phe Arg Ser Thr Arg His Asn Phe Asn Ser Met Ala Phe Pro

PC32099A\_GPR35 SERQUENCE for NY (Identical to PC32099) 170 175 165

Leu Leu Gly Phe Tyr Leu Pro Leu Ala Val Val Val Phe Cys Ser Leu 180 185

Lys Val Val Thr Ala Leu Ala Gln Arg Pro Pro Thr Asp Val Gly Gln 195 200 205

Ala Glu Ala Thr Arg Lys Ala Ala Arg Met Val Trp Ala Asn Leu Leu 210 215 220

Val Phe Val Val Cys Phe Leu Pro Leu His Val Gly Leu Thr Val Arg 225 230 235 240

Leu Ala Val Gly Trp Asn Ala Cys Ala Leu Leu Glu Thr Ile Arg Arg 250

Ala Leu Tyr Ile Thr Ser Lys Leu Ser Asp Ala Asn Cys Cys Leu Asp 260 270

Ala Ile Cys Tyr Tyr Met Ala Lys Glu Phe Gln Glu Ala Ser Ala 280 285

Leu Ala Val Ala Pro Ser Ala Lys Ala His Lys Ser Gln Asp Ser Leu 290 295 300

Cys Val Thr Leu Ala 305

<210> <211>

DNA <213> mouse

<400> 5

atgaatagta caacetgtaa cagcacecte acgtggcetg etteegteaa caacttette 60 ateatetact cageettget getggtgetg ggeetgetge teaacagegt ggeactetgg 120 gtattetget ategeatgea eeagtggaea gagaceegea tetatatgae eaacetgget 180 gtggccgacc tetgcetget etgeteettg ceatttgtge tgtactecet gaaatatagt 240 tetteagaca caccegtetg ceagetetea cagggeatet acetggeeaa cagatacatg 300 agcataagce tggteactge cattgetgtg gaccgetatg tggcagtgeg geateceetg 360 egtgegegtg agetgeggte eeegagacag getgeageag tgtgtgtgge eetttgggtg 420atagtggtca cetecetggt agtgegetgg egeetgggga tgeaggaggg tggettetge 480 tteageagee aaaceeggeg caattteage aceaetgeet teteaetget gggattetae 540 etgeegetgg ceategtggt ettetgetet ttgeaggtag tgaetgtget ategagaagg 600 ccagccgctg atgtggggca ggcagaggcc acccaaaagg ccacccacat ggtctgggcc 660 aacttggetg tgtttgteat etgetteetg eeettgeatg tggteetgae egtgeaggte 720 tecetgaace teaatacetg tgetgeeega gacacettea geegtgeeet gtecateaca 780 ggtaaactet cagacaccaa etgetgeetg gatgecatet gttactacta catggecaga 840 900 gagtteeagg aagegteeaa geeageeaeg tetteeaaea cacceacaa gageeaagat

4/8

WO 2005/085867 PCT/IB2005/000382

PC32099A\_GPR35 SERQUENCE for NY (Identical to PC32099) teceagatee tgageeteae etag 924

<210> 6 <211> 307

<212> PRT <213> mouse

<400> 6

Met Asn Ser Thr Thr Cys Asn Ser Thr Leu Thr Trp Pro Ala Ser Val 1 10 15

Asn Asn Phe Phe Ile Ile Tyr Ser Ala Leu Leu Leu Val Leu Gly Leu 25

Leu Leu Asn Ser Val Ala Leu Trp Val Phe Cys Tyr Arg Met His Gln 35 40

Trp Thr Glu Thr Arg Ile Tyr Met Thr Asn Leu Ala Val Ala Asp Leu 50 60

Cys Leu Leu Cys Ser Leu Pro Phe Val Leu Tyr Ser Leu Lys Tyr Ser 65 76 75 80

Ser Ser Asp Thr Pro Val Cys Gln Leu Ser Gln Gly Ile Tyr Leu Ala 85 90

Asn Arg Tyr Met Ser Ile Ser Leu Val Thr Ala Ile Ala Val Asp Arg 100 105

Tyr Val Ala Val Arg His Pro Leu Arg Ala Arg Glu Leu Arg Ser Pro 115 120 125

Arg Gln Ala Ala Ala Val Cys Val Ala Leu Trp Val Ile Val Val Thr 130 135 140

Ser Leu Val Val Arg Trp Arg Leu Gly Met Gln Glu Gly Gly Phe Cys 145 150 155 160

Phe Ser Ser Gln Thr Arg Arg Asn Phe Ser Thr Thr Ala Phe Ser Leu 170 175

Leu Gly Phe Tyr Leu Pro Leu Ala IIe Val Val Phe Cys Ser Leu Gln 180 185 190

Val Val Thr Val Leu Ser Arg Arg Pro Ala Ala Asp Val Gly Gln Ala 195 200 205

Glu Ala Thr Gln Lys Ala Thr His Met Val Trp Ala Asn Leu Ala Val 210 220

Phe Val Ile Cys Phe Leu Pro Leu His Val Val Leu Thr Val Gln Val 225 230 240

Ser Leu Asn Leu Asn Thr Cys Ala Ala Arg Asp Thr Phe Ser Arg Ala 250 255

Leu Ser Ile Thr Gly Lys Leu Ser Asp Thr Asn Cys Cys Leu Asp Ala

PC32099A\_GPR35 SERQUENCE for NY (Identical to PC32099)
265 270

Ile Cys Tyr Tyr Met Ala Arg Glu Phe Gln Glu Ala Ser Lys Pro

Ser Leu Thr 305

<210> 7

<211> 61 <212> DNA

<213> Artificial Sequence

260

<220>

<223> primer

<400> 7

eeggaatteg eeaceatgga ttacaaggat gaegaegata agaatggeae etacaacace

60 61

t .

<210> 8 <211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 8

tegtetagaa ttaggegagg gteaegeaca

30

<210> 9 <211> 36

<211> 30 <212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 9

ceggaatteg ceaccatgaa tggcacctac aacacc

36

<210> 10

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 10

eccegaatte gecaccatga atagtacaac etgtaacage

40

<210> 11

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 11

cccctcgag ctaggtgagg ctcaggatct ggga

34

## PC32099A\_GPR35 SERQUENCE for NY (Identical to PC32099)

<210> <211> <212> <213>	12 23 DNA Artificial Sequence	
<220> <223>	primer	
<400> teegte	12 agat gagecetagg acc	23
<210> <211> <212> <213>	13 26 DNA Artificial Sequence	
<220> <223>	primer	
<400> cacagg	13 ttee tetggeeett ggeatg	26
<210> <211> <212> <213>	14 36 DNA Artificial Sequence	
<220> <223>	primer	
<400> ccccga	14 atte gecaccatga acaatacaaa tigtag	36
<210> <211> <212> <213>	15 30 DNA Artificial Sequence	
<220> <223>	primer	
<400> cccct	15 cgag ctaggtgagg ctcaggctct	30
<210> <211> <212> <213>	16 25 DNA Artificial Sequence	
<220> <223>	primer	
<400> cactee	16 ctgc gagacacete agaca	25
<210> <211> <212> <213>	17 25 DNA Artificial Sequence	
<220> <223>	primer	
<400> tagtage	17 caga tggcgtccag geage	25
<210>	18	

WO 2005/085867 PCT/IB2005/000382

## PC32099A\_GPR35 SERQUENCE for NY (Identical to PC32099) <211> 17 <212> DNA <213> Artificial Sequence <220> <223> primer <400> 18 17 tgeaceacea actgett <210> 19 <211> 17 <212> DNA <213> Artificial Sequence <220> <223> primer <400> 19 tactccttgg aggccat 17 <210> 20 <211> 24 <212> DNA <213> Artificial Sequence <220> <223> primer <400> 20 24 aaattgtage atcctcccgt ggcc <210> 21 <211> 24 <212> DNA <213> Artificial Sequence <220> <223> primer <400> 21 tatettgget ettgtggggt gtge 24 <210> 22 <210 24 <211> 24 <212> DNA <213> Artificial Sequence <220> <223> primer <400> 22 24 gtetteacea ecatggagaa gget <210> 23 <211> 25 <212> DNA <213> Artificial Sequence <220> <223> primer

gtgatggcat ggactgtggt catga

25